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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/684,708A

DATE: 07/19/2002

TIME: 14:54:52

Input Set : A:\6240SEQ.txt

Output Set: N:\CRF3\07192002\I684708A.raw

2 <110> APPLICANT: Carroll, Steven, M.D., Ph.D
 4 <120> TITLE OF INVENTION: SMDF Neuregulin Splice Variant Isoforms and Uses
 5 Thereof
 7 <130> FILE REFERENCE: D6240
 9 <140> CURRENT APPLICATION NUMBER: US 09/684,708A
 C--> 10 <141> CURRENT FILING DATE: 2000-08-25
 12 <150> PRIOR APPLICATION NUMBER: US 60/158,622
 13 <151> PRIOR FILING DATE: 1999-10-18
 15 <160> NUMBER OF SEQ ID NOS: 27
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2856
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Rattus norvegicus
 22 <220> FEATURE:
 23 <222> LOCATION:
 24 <223> OTHER INFORMATION: Nucleotide sequence SMDF(1a cDNA (from clone pSLC135)
 26 <400> SEQUENCE: 1

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JUL 26 2002

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28 tttttcagcc gctgcgttaa cacgacagga tgctgttgct actgtcgctg ctgccctctcc 120
29 tgccgcgcgc gctgctgccg ccgccgcctc ctctggctctt gcttttgctt ttacttctcc 180
30 tgcatgacag ttgttttctt cctctaagca gacaccagct tcagacgctt gaggtgagaa 240
31 acatgccttt cagtttgga tactggttta cttaatcggc taggcggcag cttgcttcct 300
32 attttggtcc cctgccttct tgaccaaccc ggcatgggtt ggagaagcat ttgaaagaac 360
33 tgaaaaagtg tcccagaaac aacagctcaa gatatttcgg tacacttcta ttcatagtt 420
34 gctagaagcc ctttcttttt cgtttttttt ttctttttct ttttcttttt ctttttcctt 480
35 ttcttgcctt ctcctaagct ctggtacttt gggttaattgc cttggacttg ggtgccttat 540
36 cgatttcccc ctccaagatg ctgtatcatt tgggtggggg gagctctgcg tggtaatgca 600
37 ctgtgagaga ggccaggcct tctggaggty agccgatgga gatttattcc ccagacatgt 660
38 ctgaggtagc tggcgggagg tctccagcc cctccactca gctgagtga gcccatctc 720
39 ttgatgggct tccggcagcg gaggaacata taccagacac ccacacagaa gatgagagaa 780
40 gccctggact cctgggcctg gcggtgccct gctgtgtgtg cctggaagct gagcgctga 840
41 gaggggtgtc caactccgag aagatctgca ttgttcccat tctggcttgc ctagtcagcc 900
42 tctgcctctg cattgctggc ctgaagtggg tatttgtgga caagatattt gaatacgact 960
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47 caccgccctt cccttctcca gctcggaccc ctgagggtgag aacacccaag tcaggaactc 1260
48 agccacaaac aacagaaact aacctgcaaa ctgtctctaa actttccaca tcgacatcca 1320
49 cgactgggac cagccatctc ataaagtgcg cggagaagga gaaaactttc tgtgtgaatg 1380
50 gggcgagtg cttcacggtg aaggacctgt caaaccgctc aagatacttg tgcaagtgcc 1440
51 caaatgagtt tactggtgat cgttgccaaa actacgtaat ggccagcttc tacaagcatc 1500
52 ttgggattga atttatggaa gcggagggaac tctaccagaa gaggggtgctg acaattactg 1560

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53 gcacgtgtat cgccctgctg gtgggtcgga tcatgtgtgt ggtggcctac tgcaaaacca 1620
54 agaagcagcg gcagaagctt catgatcggc ttcggcagag tcttcggtca gaacggagca 1680
55 acctggtgaa catagcgaat gggcctcacc acccaaaccg gccgccagag aacgtgcagc 1740
56 tggatgaatca atacgtatct aaaaacgtca tctccagtga gcatattgtt gagagagaag 1800
57 tggagacttc cttttccacc agtcattaca cttccacagc ccatcactcc acgactgtca 1860
58 cccagactcc tagtcacagc tggagtaatg ggcacacgga gagcgctatt tcagaaagca 1920
59 actccgtaat catgatgtct tcggtagaga acagcaggca cagcagtccc gccggggggc 1980
60 caccgaggacg tcttcatggc ctgggaggcc ctctgtataa cagcttcctc aggcattgca 2040
61 gagaaacccc tgactcctac agagactctc ctcatagcga aaggatgtga tcagccatga 2100
62 ccaccccgcc tcgtatgtca cctgtagatt tccacacgcc aagctccctc aaatcgcccc 2160
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65 agaaatatga tcatcaccgc cagcaactca actcctttca tcacaaccct gcacatcaga 2340
66 gtaccagcct ccccccctagc ccactgagga tagtggagga tgaggagtac gagacgaccc 2400
67 aggagtatga gtcagttcaa gagcccggtt agaaagtcac caatagccgg cgggccaaaa 2460
68 gaaccaagcc caatggccac attgccaaata ggttggaat ggacagcaac acaagttctg 2520
69 tgagcagtaa ctcagaaagt gagacagaag acgaaagagt aggtgaagac acaccattcc 2580
70 tgggcataca gaacccctg gcagccagcc ttgaggtggc ccccgcttc cgtctggctg 2640
71 agagcaggac taaccacga ggcgcttct ccacacagga ggaattacag gccaggctgt 2700
72 ctagtgtaat cgctaaccga gaccctattg ctgtataaaa cctaaataaa cacatagatt 2760
73 caccgtgaaa actttatttt atataataaa gtatttcacc ttaaattaaa caattttatt 2820
74 tatttttagca gttctgcaaa tactcgtgcc gaattc 2856

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76 <210> SEQ ID NO: 2

77 <211> LENGTH: 700

78 <212> TYPE: PRT

79 <213> ORGANISM: Rattus norvegicus

81 <220> FEATURE:

82 <223> OTHER INFORMATION: Amino acid sequence of SMDF(1a (encoded by

83 clone pSLC135)

85 <400> SEQUENCE: 2

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86 Met Glu Ile Tyr Ser Pro Asp Met Ser Glu Val Ala Gly Gly Arg
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89 Ser Ser Ser Pro Ser Thr Gln Leu Ser Ala Ala Pro Ser Leu Asp
90      20      25      30
92 Gly Leu Pro Ala Ala Glu Glu His Ile Pro Asp Thr His Thr Glu
93      35      40      45
95 Asp Glu Arg Ser Pro Gly Leu Leu Gly Leu Ala Val Pro Cys Cys
96      50      55      60
98 Val Cys Leu Glu Ala Glu Arg Leu Arg Gly Cys Leu Asn Ser Glu
99      65      70      75
101 Lys Ile Cys Ile Val Pro Ile Leu Ala Cys Leu Val Ser Leu Cys
102      80      85      90
104 Leu Cys Ile Ala Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe
105      95     100     105
107 Glu Tyr Asp Ser Pro Thr His Leu Asp Pro Gly Gly Leu Gly Gln
108     110     115     120
110 Asp Pro Val Ile Ser Leu Asp Pro Thr Ala Ala Pro Ala Ile Leu
111     125     130     135
113 Val Ser Ser Glu Ala Tyr Thr Ser Pro Val Ser Lys Ala Gln Ser

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| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| 114 | | 140 | | 145 | | 150 |
| 116 | Glu | Ala | Gly | Ala | His | Val |
| 117 | | 155 | | 160 | | 165 |
| 119 | Ala | Ser | Glu | Pro | Ser | Ala |
| 120 | | 170 | | 175 | | 180 |
| 122 | Ala | Phe | Pro | Pro | Phe | His |
| 123 | | 185 | | 190 | | 195 |
| 125 | Ala | Arg | Thr | Pro | Glu | Val |
| 126 | | 200 | | 205 | | 210 |
| 128 | Gln | Thr | Thr | Glu | Thr | Asn |
| 129 | | 215 | | 220 | | 225 |
| 131 | Ser | Thr | Ser | Thr | Thr | Gly |
| 132 | | 230 | | 235 | | 240 |
| 134 | Lys | Glu | Lys | Thr | Phe | Cys |
| 135 | | 245 | | 250 | | 255 |
| 137 | Lys | Asp | Leu | Ser | Asn | Pro |
| 138 | | 260 | | 265 | | 270 |
| 140 | Glu | Phe | Thr | Gly | Asp | Arg |
| 141 | | 275 | | 280 | | 285 |
| 143 | Tyr | Lys | His | Leu | Gly | Ile |
| 144 | | 290 | | 295 | | 300 |
| 146 | Gln | Lys | Arg | Val | Leu | Thr |
| 147 | | 305 | | 310 | | 315 |
| 149 | Val | Val | Gly | Ile | Met | Cys |
| 150 | | 320 | | 325 | | 330 |
| 152 | Gln | Arg | Gln | Lys | Leu | His |
| 153 | | 335 | | 340 | | 345 |
| 155 | Glu | Arg | Ser | Asn | Leu | Val |
| 156 | | 350 | | 355 | | 360 |
| 158 | Asn | Pro | Pro | Pro | Glu | Asn |
| 159 | | 365 | | 370 | | 375 |
| 161 | Lys | Asn | Val | Ile | Ser | Ser |
| 162 | | 380 | | 385 | | 390 |
| 164 | Thr | Ser | Phe | Ser | Thr | Ser |
| 165 | | 395 | | 400 | | 405 |
| 167 | Thr | Thr | Val | Thr | Gln | Thr |
| 168 | | 410 | | 415 | | 420 |
| 170 | Thr | Glu | Ser | Val | Ile | Ser |
| 171 | | 425 | | 430 | | 435 |
| 173 | Ser | Val | Glu | Asn | Ser | Arg |
| 174 | | 440 | | 445 | | 450 |
| 176 | Gly | Arg | Leu | His | Gly | Leu |
| 177 | | 455 | | 460 | | 465 |
| 179 | Arg | His | Ala | Arg | Glu | Thr |
| 180 | | 470 | | 475 | | 480 |
| 182 | Ser | Glu | Arg | Tyr | Val | Ser |
| 183 | | 485 | | 490 | | 495 |
| 185 | Pro | Val | Asp | Phe | His | Thr |
| 186 | | 500 | | 505 | | 510 |

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Output Set: N:\CRF3\07192002\I684708A.raw

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188 Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser
189                               515                               520                               525
191 Val Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu
192                               530                               535                               540
194 Val Thr Pro Pro Arg Leu Arg Glu Lys Lys Tyr Asp His His Pro
195                               545                               550                               555
197 Gln Gln Leu Asn Ser Phe His His Asn Pro Ala His Gln Ser Thr
198                               560                               565                               570
200 Ser Leu Pro Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr
201                               575                               580                               585
203 Glu Thr Thr Gln Glu Tyr Glu Ser Val Gln Glu Pro Val Lys Lys
204                               590                               595                               600
206 Val Thr Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His
207                               605                               610                               615
209 Ile Ala Asn Arg Leu Glu Met Asp Ser Asn Thr Ser Ser Val Ser
210                               620                               625                               630
212 Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val Gly Glu Asp
213                               635                               640                               645
215 Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser Leu Glu
216                               650                               655                               660
218 Val Ala Pro Ala Phe Arg Leu Ala Glu Ser Arg Thr Asn Pro Ala
219                               665                               670                               675
221 Gly Arg Phe Ser Thr Gln Glu Glu Leu Gln Ala Arg Leu Ser Ser
222                               680                               685                               690
224 Val Ile Ala Asn Gln Asp Pro Ile Ala Val
225                               695                               700
227 <210> SEQ ID NO: 3
228 <211> LENGTH: 296
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Amino acid sequence of human SMDF(3
235 <400> SEQUENCE: 3
237 Met Glu Ile Tyr Ser Pro Asp Met Ser Glu Val Ala Ala Glu Arg
238                               5                               10                               15
240 Ser Ser Ser Pro Ser Thr Gln Leu Ser Ala Asp Pro Ser Leu Asp
241                               20                               25                               30
243 Gly Leu Pro Ala Ala Glu Asp Met Pro Glu Pro Gln Thr Glu Asp
244                               35                               40                               45
246 Gly Arg Thr Pro Gly Leu Val Gly Leu Ala Val Pro Cys Cys Ala
247                               50                               55                               60
249 Cys Leu Glu Ala Glu Arg Leu Arg Gly Cys Leu Asn Ser Glu Lys
250                               65                               70                               75
252 Ile Cys Ile Val Pro Ile Leu Ala Cys Leu Val Ser Leu Cys Leu
253                               80                               85                               90
255 Cys Ile Ala Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu
256                               95                               100                              105
258 Tyr Asp Ser Pro Thr His Leu Asp Pro Gly Gly Leu Gly Gln Asp
259                               110                              115                              120

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261 Pro Ile Ile Ser Leu Asp Ala Thr Ala Ala Ser Ala Val Trp Val
262                               125                130                135
264 Ser Ser Glu Ala Tyr Thr Ser Pro Val Ser Arg Ala Gln Ser Glu
265                               140                145                150
267 Ser Glu Val Gln Val Thr Val Gln Gly Asp Lys Ala Val Val Ser
268                               155                160                165
270 Phe Glu Pro Ser Ala Ala Pro Thr Pro Lys Asn Arg Ile Phe Ala
271                               170                175                180
273 Phe Ser Phe Leu Pro Ser Thr Ala Pro Ser Phe Pro Ser Pro Thr
274                               185                190                195
276 Arg Asn Pro Glu Val Arg Thr Pro Lys Ser Ala Thr Gln Pro Gln
277                               200                205                210
279 Thr Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser
280                               215                220                225
282 Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys
283                               230                235                240
285 Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys
286                               245                250                255
288 Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu
289                               260                265                270
291 Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr
292                               275                280                285
294 Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
295                               290                295

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297 <210> SEQ ID NO: 4

298 <211> LENGTH: 2540

299 <212> TYPE: DNA

300 <213> ORGANISM: Rattus norvegicus

302 <220> FEATURE:

303 <221> NAME/KEY: CDS

304 <222> LOCATION: 370..2458

305 <223> OTHER INFORMATION: SMDF_2a amino acid sequence

307 <400> SEQUENCE: 4

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310 agatatttcg gtacatttct atttcatagt tgctagaagc cttttctttt ttcgtttttt 180
311 ttttttcttt ttctttttct ttttcttttt ctttttcttg ctctctccta agctctggta 240
312 ctttgggtaa ttgccttgga cttgggtgcc ttatcgattt cccctccaa gatgctgtat 300
313 catttggttg gggggagctc tgcgtggtaa tgcactgtga gagaggccag gccttctgga 360
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316 catataccag acacccacac agaagatgag agaagccctg gactcctggg cctggcggtg 540
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318 tgcattgttc ccattctggc ttgcctagtc agcctctgcc tctgcattgc tggcctgaag 660
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322 gtacaagggt accatgctgc tgtggcctct gaaccttcag cagtaccgac ccggaagaac 900
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VERIFICATION SUMMARY

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Input Set : A:\6240SEQ.txt

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L:680 M:283 W: Missing Blank Line separator, <400> field identifier